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GenCore version 5.1.3

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	5.5	1.2	2.1	B1052878	H:95-2878 RC5-GH024
	2	6.5	1.20	B1054415	B1044756 RC5-GH024
1, c	3	6.5	1.30	B10367833	BQ757833 RC5-GH024
1, c	4	6.5	1.65	B10454542	BG7574542 E0274194
5	5	6.5	1.50	B10844124	BM844124 K-EST0124
6	6	6.5	1.60	B10844123	BF8041323 QV4-C101
7	7	6.5	1.60	B10845219	AW85219 CM0-C100
c	8	6.5	1.60	B10845219	BW85219 CM0-C100
c	9	6.5	1.60	B10845219	BW85219 CM0-C100
c	10	6.5	1.60	B10845219	BW85219 CM0-C100
c	11	6.5	1.60	B10845219	BW85219 CM0-C100
c	12	6.5	1.60	B10845219	BW85219 CM0-C100
c	13	6.5	1.60	B10845219	BW85219 CM0-C100
c	14	6.5	1.60	B10845219	BW85219 CM0-C100
c	15	6.5	1.60	B10845219	BW85219 CM0-C100
16	6.5	1.60	4.47	AW97331	AW97331 RC2-BN004
17	6.5	1.60	4.54	B1050019	B1050019 CM2-GN024
18	6.5	1.60	4.60	B10846053	BM846053 K-FSU10124
19	6.5	1.60	4.69	B10844242	A1834242 PC0-H1001
20	6.5	1.60	4.81	B10846715	BH10846715 PC0-GNU001
21	6.5	1.60	4.92	BG367835	BQ367835 RC5-GH024
22	6.5	1.60	4.84	BW852115	AW852115 CM0-C100
23	6.5	1.60	4.84	B10149416	BE10149416 60144009
24	6.5	1.60	4.84	B10834308	BM84209 K-EST0109
25	6.5	1.60	4.90	B1056723	BIG56723 RC5-GN024
26	6.5	1.60	4.96	BH785233	BH785233 K-IRS1006
27	6.5	1.60	5.07	B10820595	BH10820595 K-EST001
28	6.5	1.30	5.43	A1046402	AI046402 K-BT1008
29	6.5	1.00	5.60	B10786594	BM786594 K-EST006
30	6.5	1.00	6.41	B107861280	BM7861280 K-EST004
31	6.5	1.30	5.53	B107862914	BM7862914 K-LS1654
32	6.5	1.90	5.64	B27456742	BG7556742 60273380
33	6.5	1.90	5.64	B10784565	BM784565 K-EST001
34	6.5	1.00	5.72	B1044665	BE29543 601742034
35	6.5	1.00	5.74	B10785935	BM785935 K-EST006
36	6.5	1.00	5.83	B10843500	BM7843500 K-EST006
37	6.5	1.00	5.90	B10784604	BM784604 K-EST004
38	6.5	1.00	5.92	B10740978	BM740978 K-EST001
39	6.5	1.00	5.93	B10838153	BH638153 K-EST011
40	6.5	1.00	6.15	B1060897	BI060897 60273383
41	6.5	1.00	6.22	B10785140	BM785140 K-EST006
42	6.5	1.00	6.22	B10783755	BM783755 K-EST004
43	6.5	1.00	6.32	B10787345	BM787345 K-EST004
44	6.5	1.00	6.34	B10693854	AW93854 RC3-BN003
45	6.5	1.00	6.42	B10701919	BE10701919 bb673033
	6.5	100	6.97	AU141534	AU141534 AU141534

AUGUST 1975

Alignment Scores:	
Prod. No.:	0_0016
Score:	65.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Quer., Match:	—C— DB;
DB:	14
US-09-856-070-19 (1-13) x HQ367833 (1-215)	
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BIG5754562	234 bp tRNA LINEAR EST 15 MAY 2007
Locus	6.0271194F1 NIH-MFR-48 Homo sapiens cDNA clone IMAGE:4R466305'.
DEFINITION	mRNA sequence.
ACCESSION	HC754562
VERSION	BG754562.1
KEYWORDS	EST.
ORGANISM	human.
SOURCE	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 234)
AUTHORS	NIH-MC http://mcg.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert J. Strausberg, PhD
JOURNAL	

Email: crabs@mail.nih.gov
Tissue procurement: Louis M. Shultz, M.D.,
DNA library preparation: Ling Hong/Rubin laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGIC clone distribution information can be
found through the I.M.A.G.E. Consortium (LLNL) et al.

BASE COUNT
ORIGIN
81 a 38 c 96 q 19 t
NOTE: this is a NH₂MGC library.

Alignment scores:					
Pred. No.:	0.00181	length:	234		
Score:	65.00	Matches:	13		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Deletes:	0		
DB:	12	Inserts:	0		
		gaps:	0		

US-09-856-079-19 (1-13) x BC754562 (1-234)
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 27

RESULT 5
B#844124

LOCUS BM844124 **DEFINITION** KESTRELLAISI 5'-GAGG...-3' mRNA sequence
ACCESSION BM844124 **VERSION** 1 **UPDATE** 2009-03-05
ORGANISM *Candidatus Styraxiphilus* **MATERIAL** leaf sap from *Styrax obassia*
DBSOURCE NCBI **COMMENT** This is the first complete genome sequence of a member of the genus *Kestrella*.

KEYWORDS EST, human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Choi, M.Y., Kim, M.R., Ch, K.T., Cheong, J.E., Suh, H.Y., Kim, J.M., Park, H.S., Kim, S., and **EDITOR** Cho, M.J.

TITLE 21C Frontier Korean EST Project, 2001
JGSAI Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eojeon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel : +82-42-860-4470
Fax : +82-42-860-4409

plate: 18 row: G column: 03
High quality sequence stop: 275.
Location/Qualifiers
1 .. 275

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="SL3KMS5-38-G03"
/clone_id="SL3KMS5"

/tissue-type-myeloma
 /cell-line-RMS-5*
 /lab_host="topof"
 /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly(A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then de-carried with trichloroacetic acid pyrophosphatase (TAP). The decapped viral mRNA was linked with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with detailed vector. The detailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. Ac RNA strand converted to a DNA strand by Okazawa Berg method. The obtained cDNA vectors

top10F' by electroporation method. the cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 81 a library

ORIGIN

Alignment Scores:
pred. No.: 0.00227
Score: 65.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 14

US-09-856-070-19 (1-13) x 18844124 (1-275)

QY 1 LysglugluMetLeuArgLeuGlnAspTyrIgluL 14
1b 45 AAGTAGATTCAGCTGGCGCCGAGCAGAACAGAG 94

RESULT 6

BF804_324

DEFINITION BF804_324

VERSION BF804_324.1

FST

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 281)

ACTORS Dias Neto, R., Gai, I., Correa, K., Vojtovský, Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W., Jr., Zago, M.A., Bordin, S., Costa, F.E.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baird, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, I.F., de Souza, S.J., and

Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT MEDLINE

CONTACT Simpson, A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antônio Prudente 100, 4 andar, 01050-010, São Paulo, SP,

Brazil

Phone: +55 11 2764922

Fax: +55 11 2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ncbi.nlm.nih.gov/blast/blast.cgi?db=HCCP&format=html&query=BF804_324)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 280.

FEATURES Source

Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

/clone_lib="C100/2"

/dev_stage="Adult"

/note="cDNA: vector: puc 18 vector, reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Site 1: Shal: A minilibRARY was made by cloning products

derived from cRESTES PCR (HS Letters Patient application

No. 140,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

Site 2: Shal: A minilibRARY was made by cloning products

derived from cRESTES PCR (HS Letters Patient application

No. 140,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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stringency conditions."

Source

Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

/clone_lib="C100/2"

/dev_stage="Adult"

/note="cDNA: vector: puc 18 vector, reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

Site 1: Shal: A minilibRARY was made by cloning products

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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stringency conditions."

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Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

/clone_lib="C100/2"

/dev_stage="Adult"

/note="cDNA: vector: puc 18 vector, reverse transcription of tissue

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Site 1: Shal: A minilibRARY was made by cloning products

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

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stringency conditions."

Source

Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

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/note="cDNA: vector: puc 18 vector, reverse transcription of tissue

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

/clone_lib="C100/2"

/dev_stage="Adult"

/note="cDNA: vector: puc 18 vector, reverse transcription of tissue

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No. 140,716 - Ludwig Institute for Cancer Research) profiles

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derived from cRESTES PCR (HS Letters Patient application

No. 140,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

Source

Length: 279

Organism: "Homo sapiens"

/db_xref="LICR Human Cancer Genome Project"

/clone_lib="C100/2"

/dev_stage="Adult"

/note="cDNA: vector: puc 18 vector, reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

Site 1: Shal: A minilibRARY was made by cloning products

derived from cRESTES PCR (HS Letters Patient application

No. 140,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

Site 2: Shal: A minilibRARY was made by cloning products

US-09-856-070-19 (1-13) x AW845219 (1-281)

QY 1 LysCluGluLeuMetLeuArgLeuGlnAspTyrGlnGlu 13
DB 173 AAGGGAGCTAATGCTGGCTGACATATGACAG 211

RESULT 8
BL05028/c

LOCUS BL05028 294 bp mRNA linear EST 15-JUN-2001
DEFINITION CM2-00294-070101-675-p08-E0148 mRNA
ACCESSION BL05028
VERSION BL05028_1 G1:14457558

KEYWORDS EST, human

SOURCE Human sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Vertebrata; Euteleostomi; Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 294)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordim,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bajaj,G.S., Simpson,D.H., Brustein,A., de oliveira,P.S., Butcher,P., Toneneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.P., Reis,J.F., de Souza,S.J., and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Ludwig Institute for Cancer Research
Boa Prof. Antonio Prudente 109, 4 andar, 01500-010, Sao Paulo-SP, Brazil
Tel: +55-11-2764722
Fax: +55-11-2767001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICK Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/crestes/p4-phm2/p181.html?db=GN0294>).
Seq. Primer: puc18 forward
High quality sequence start: 17
High quality sequence stop: 294.
Location/Qualifiers J..294..
Source /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0294"
/dev_stage="Adult"
/note="vector: placent-a-normal; vector: puc18; site_1: small products derived from QRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the FUC 18 vector; reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES source
BASE COUNT 34 a 114 c 56 g 90 t
ORIGIN
Alignment Scores:
Pred. No.: 6 60249
Score: 65.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 13
DB: 13

RESULT 9
BF669430

LOCUS BF669430 294 bp mRNA linear EST 17 JAN 2001
DEFINITION QV0-E10148-231000-456-d07 ET0148 Homo sapiens cDNA, mRNA sequence.
ACCESSION HF869430
VERSION HF869430_1 G1:12259560
KEYWORDS EST, human

ORGANISM Human sapiens

Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 297)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordim,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bajaj,G.S., Simpson,D.H., Brustein,A., de oliveira,P.S., Butcher,P., Toneneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.P., Reis,J.F., de Souza,S.J., and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Ludwig Institute for Cancer Research
Boa Prof. Antonio Prudente 109, 4 andar, 01500-010, Sao Paulo-SP, Brazil
Tel: +55-11-2764722
Fax: +55-11-207001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICK Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/crestes/p4-phm2/p181.html?db=GN0294-1>)
Seq. Primer: puc18 forward
High quality sequence stop: 297.
Location/Qualifiers J..297..
Source /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0148"
/dev_stage="Adult"
/note="vector: placent-a-normal; vector: puc18; site_1: small products derived from QRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the FUC 18 vector; reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES source
BASE COUNT 90 a 56 c 119 g 31 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 0 00253
Score: 65.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 12
DB: 12

RESULT 10
BM827086

LOCUS BM827086 312 bp mRNA linear EST 06-MAR-2002
DEFINITION P EST060421-SYSN01 Human cDNA mRNA sequence.
ACCESSION BM827086

QY 1 LysCluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 13
DB 216 AACGAGCTAATGCTGGCTGACATATGACAG 178

US-09-856-070-19 (1-14) x BL05028 (1-294)

VERSION: NM_27061_GI:19183495
 EST: human
 SOURCE: NCBI
 ORGANISM: Homo sapiens
 FEATURES:
 REFERENCE: Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS: Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Song, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 TITLE: Unpublished (2002)
 JOURNAL: 21st Frontier Korean EST Project 2001
 COMMENT: Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52, Exeung-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsu@kribb.re.kr
 Plate: 4 row: G column: 09
 High quality sequence stop: 312.
 Location/Qualifiers
 1..312
 /organism="Homo sapiens"
 /db_xref="Taxon:9606"
 /clone="SGSNW601A-009"
 /clone_id="SGSNW601A-009"
 /sex="M"
 /issue_type="Assembly"
 /cell_line="Epithelial"
 /cell_line_id="SNJ601"
 /lab="Mestech"
 /lab_id="TopOf"
 /note="Human stomach Vector: pME18-FL3; site_1: XbaI; Site_2: XbaI; The first (A+) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped linear intact mRNA was ligated with RNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into blatt- digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
 BASE COUNT: 108 a 60 c 110 g 34 t
 ORIGIN: RESULT 11
 Alignment Scores:
 Pred. No.: 0.00271 Length: 312
 Score: 65.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 OS: 09 856 070-19 (1 13) x NM_27061_GI:19183495 (1-312)
 LOCUS: HQ323837 LINEAR mRNA linear EST 17-MAY-2002
 DEFINITION: CM0-C1095-301000-648-P05 clones Homo sapiens cDNA, mRNA sequence
 ACCESSION: HQ323837
 VERSION: 1
 KEYWORDS: EST, human, Homo sapiens
 SOURCE: NCBI
 ORGANISM: Homo sapiens
 FEATURES:
 REFERENCE: Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS: Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britto, F.P., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordio, S., Costa, F.F., Simpson, D.H., Goldman, C.H., Carvalho, A.P., Matsunaga, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Burcher, P., Jongeneel, C.V., de Souza, S.J. and Simpson, A.J.
 TITLE: Shotgun sequencing of the human transcriptome with cDNA expressed sequence tags
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT: Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antônio Prudente 169, 4 andar, 01509-010, São Paulo, SP, Brazil
 Tel: 55 11 2764922
 Fax: 55 11 27649001
 Email: ajsimpson@ludwig.org.br
 This sequence was derived from the EAPESP/LICR Human Cancer Genome project. This entry can be seen in the EAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/qgenomic2.pl?11-CM052-EMO_C1095-301000-648-hos5g*3-2000-10-30t4-1)
 Seq. primer: puc 18 forward
 High quality sequence stop: 2.
 Location/Qualifiers
 1..358
 /organism="Homo sapiens"
 /db_xref="Caxon:9606"
 /clone_id="C1095-301000-648-hos5g*3-2000-10-30t4-1"
 /dev_stage="Adult"
 /note="cDNA cloning vector, published Site 1: Sma I; Site 2: Sma I; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters patent application No. 196,716 - ludwig Institute for Cancer Research) profits into the EUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT: 112 a 74 c 130 g 42 t
 ORIGIN: RESULT 12
 Alignment Scores:
 Pred. No.: 0.00329 Length: 358
 Score: 65.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 OS: 09 856 070-19 (1-14) x BQ324837 (1-358)
 LOCUS: HQ368118 LINEAR mRNA linear EST 31-MAY-2002
 DEFINITION: CM0-C1095-301000-648-P05 clones Homo sapiens cDNA, mRNA sequence
 ACCESSION: HQ368118
 VERSION: BQ368118 1
 KEYWORDS: EST, human, Homo sapiens
 SOURCE: NCBI
 ORGANISM: Homo sapiens
 FEATURES:
 REFERENCE: Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS: Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britto, F.P., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordio, S., Costa, F.F., Goldman, C.H., Carvalho, A.P., Matsunaga, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Burcher, P., Jongeneel, C.V., de Souza, S.J. and Simpson, A.J.

M.J. Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.T. and

Simpson, A.J.G. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.

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Rua Prof. Antônio Prudente 109, 4 andar, 01509 010, São Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2737001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LUDWIG Human Cancer Genome project, this entry can be seen in the following URL:

(<http://www.ludwig.org.br/scripts/geneinfo?P=13105&G=14-1>)

seq primer: puc 18 forward

High quality sequence start: 11

High quality sequence stop: 348.

Location/Qualifiers

1. .364 alignment; Vector: puc18; Site_1: Shai

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="GN0516"

/dev_stage="Adult"

/note="Organ: placenta-notimal"; Vector: puc18; Site_1: Shai

; Site_2: Small; A mini-library was made by cloning

products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the PUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT

112 a 14 e 3 42 t

ORIGIN

Alignment Scores:

Pred. No.: 0.00337

Score: 65.30

Length: 364

Matches: 13

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 6

DB: 14

RESULT 13

US-09-856-070-19 (1-13) x BQ368118 (1-364)

QY 1 LysgluLglutLeuMetLeuAlaLysLysAspTyrGluGlu 13

Db 119 AACGAAGCTTGATGGCTGATGATGATGATGAGGAG 157

KEYWORDS

human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Crustacea; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo,

M. J. Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.T. and

Najai, M.A., da Silveira, W., Júnior, Bento, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.J., Matsukuma, A., Baita, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Burher, P., Tongen, C.V., Haro,

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

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JOURNAL

2020263

MEDLINE

COMMENT

